



SEQUENCE LISTING

<110> John, Varghese
Sinha, Sukanto
Tung, Jay

<120> BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS

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<141> 2000-12-02

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<211> 32
<212> DNA

<213> Homo sapiens

<400> 49

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32

<210> 50

<211> 11

<212> PRT

<213> Homo sapiens

<400> 50

Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
1 5 10

<210> 51

<211> 5

<212> PRT

<213> Homo sapiens

<400> 51

Val Asn Leu Asp Ala
1 5

<210> 52

<211> 9

<212> PRT

<213> Artificial

<220>

<223> Synthetic oligopeptide substrate

<400> 52

Ser Glu Val Asn Leu Asp Ala Glu Phe
1 5

<210> 53

<211> 30

<212> PRT

<213> Artificial

<220>

<223> Synthetic oligopeptide substrate

<400> 53

Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile
1 5 10 15

Lys Thr Glu Glu Ile Ser Glu Val Asn Leu Asp Ala Glu Phe
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<210> 54

<211> 5
<212> PRT
<213> Homo sapiens

<400> 54

Val Lys Met Asp Ala
1 5

<210> 55
<211> 24
<212> PRT
<213> Homo sapiens

<400> 55

Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
1 5 10 15

Glu Met Val Asp Asn Leu Arg Gly
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<210> 56
<211> 15
<212> PRT
<213> Homo sapiens

<400> 56

Ile Ser Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg
1 5 10 15

<210> 57
<211> 419
<212> PRT
<213> Homo sapiens

<400> 57

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
 325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
 340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
 355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
 370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
 385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
 405 410 415

Val Ser Ala

<210> 58
 <211> 407
 <212> PRT
 <213> Homo sapiens

<400> 58

Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
 1 5 10 15

Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val
 20 25 30

Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp
 35 40 45

Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu
 50 55 60

His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg
 65 70 75 80

Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu
 85 90 95

Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg

100					105					110					
Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly
		115					120					125			
Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg
	130					135					140				
Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr
145					150					155					160
His	Val	Pro	Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro
				165					170					175	
Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile
			180					185					190		
Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro
		195					200					205			
Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile
	210					215					220				
Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys
225					230					235					240
Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val
				245					250					255	
Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys
			260					265					270		
Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala
		275					280					285			
Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met
	290					295					300				
Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln
305					310					315					320
Tyr	Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr
				325					330					335	
Lys	Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val
			340					345					350		

Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile
 355 360 365

Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala
 370 375 380

Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr
 385 390 395 400

Asn Ile Pro Gln Thr Asp Glu
 405

<210> 59
 <211> 452
 <212> PRT
 <213> Homo sapiens

<400> 59

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
 1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
 20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
 35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
 115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
 130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
 180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
 195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
 210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
 225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
 245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
 260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
 275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
 290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
 305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
 325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
 340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
 355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
 370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
 180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
 195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
 210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
 225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
 245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
 260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
 275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
 290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
 305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
 325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
 340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
 355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
 370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
 385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
 405 410 415

Val Ser Ala Cys
 420

<210> 61
 <211> 7
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic peptide inhibitor

<220>
 <221> MISC_FEATURE
 <222> (1)..(7)
 <223> Xaa = hydroethylene

<400> 61

Glu Val Met Xaa Ala Glu Phe
 1 5

<210> 62
 <211> 26
 <212> PRT
 <213> Homo sapiens

<400> 62

Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe Met
 1 5 10 15

Leu Pro Leu Cys Leu Met Val Cys Gln Trp
 20 25

<210> 63
 <211> 33
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(33)
 <223> P26-P4'sw peptide substrate

<400> 63

Cys Gly Gly Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu

1 5 10 15

Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Asn Leu Asp Ala Glu
 20 25 30

Phe

<210> 64
 <211> 29
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(29)
 <223> P26-P1' peptide substrate with CGG linker

<400> 64

Cys Gly Gly Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu
 1 5 10 15

Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Asn Leu
 20 25

<210> 65
 <211> 501
 <212> PRT
 <213> Homo sapiens

<400> 65

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
 1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
 20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
 35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
 115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
 130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
 180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
 195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
 210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
 225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
 245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
 260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
 275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
 290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
 305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
 325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
 340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
 355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
 370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
 385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
 405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
 420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
 435 440 445

Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
 450 455 460

Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
 465 470 475 480

Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp
 485 490 495

Ile Ser Leu Leu Lys
 500

<210> 66
 <211> 480
 <212> PRT
 <213> Homo sapiens

<400> 66

Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala
 1 5 10 15

Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu
 20 25 30

Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly

		35				40						45				
Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu	Met	Thr	Val	Gly	Ser	Pro	Pro	
	50					55					60					
Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	
65					70					75					80	
Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	
				85					90					95		
Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val	Tyr	Val	Pro	Tyr	Thr	
			100					105					110			
Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp	Leu	Val	Ser	Ile	Pro	
		115					120					125				
His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu	
	130					135					140					
Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly	
145					150					155					160	
Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe	
				165					170					175		
Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	Val	Pro	Asn	Leu	Phe	Ser	Leu	
			180					185					190			
Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	
		195					200					205				
Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	
	210					215					220					
Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	
225					230					235					240	
Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	
				245					250					255		
Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	
			260					265					270			
Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	
		275					280					285				

Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly
 290 295 300

Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe
 305 310 315 320

Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe
 325 330 335

Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val
 340 345 350

Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser
 355 360 365

Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val
 370 375 380

Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His
 385 390 395 400

Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr
 405 410 415

Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
 420 425 430

Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe
 435 440 445

Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg Cys
 450 455 460

Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp Ile Ser Leu Leu Lys
 465 470 475 480

<210> 67
 <211> 444
 <212> PRT
 <213> Homo sapiens

<400> 67

Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln
 1 5 10 15

Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn
 20 25 30

Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro
 35 40 45

His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr
 50 55 60

Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp
 65 70 75 80

Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn
 85 90 95

Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe
 100 105 110

Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala
 115 120 125

Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu
 130 135 140

Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly
 145 150 155 160

Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
 165 170 175

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
 180 185 190

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
 195 200 205

Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
 210 215 220

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
 225 230 235 240

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
 245 250 255

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val

260	265	270
Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser		
275	280	285
Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile		
290	295	300
Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln		
305	310	315
Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val		
	325	330
Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala		
	340	345
Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu		
	355	360
Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu		
	370	375
Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr		
385	390	395
Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu		
	405	410
Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln		
	420	425
		430
His Asp Asp Phe Ala Asp Asp Ile Ser Leu Leu Lys		
	435	440
<210> 68		
<211> 395		
<212> PRT		
<213> Homo sapiens		
<400> 68		
Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln		
1	5	10
Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn		
	20	25
		30

Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	35	40	45
His	Pro	Phe	Leu	His	Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	50	55	60
Arg	Asp	Leu	Arg	Lys	Gly	Val	Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	65	70	75
Glu	Gly	Glu	Leu	Gly	Thr	Asp	Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	85	90	95
Val	Thr	Val	Arg	Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	100	105	110
Phe	Ile	Asn	Gly	Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	115	120	125
Glu	Ile	Ala	Arg	Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	130	135	140
Val	Lys	Gln	Thr	His	Val	Pro	Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	145	150	155
Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	165	170	175
Ser	Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	180	185	190
Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	195	200	205
Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	210	215	220
Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	225	230	235
Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	245	250	255
Ser	Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	260	265	270

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
 275 280 285

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
 290 295 300

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
 305 310 315 320

Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
 325 330 335

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
 340 345 350

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
 355 360 365

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
 370 375 380

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu
 385 390 395

<210> 69
 <211> 439
 <212> PRT
 <213> Homo sapiens

<400> 69

Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu
 1 5 10 15

Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr
 20 25 30

Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His
 35 40 45

Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys
 50 55 60

Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly
 65 70 75 80

Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala
 85 90 95

Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser
 100 105 110

Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro
 115 120 125

Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His
 130 135 140

Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu
 145 150 155 160

Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly
 165 170 175

Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile
 180 185 190

Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn
 195 200 205

Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser
 210 215 220

Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe
 225 230 235 240

Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe
 245 250 255

Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly
 260 265 270

Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly
 275 280 285

Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr
 290 295 300

Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys
 305 310 315 320

Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile
 325 330 335

Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly
340 345 350

Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala
355 360 365

Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn
370 375 380

Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met
385 390 395 400

Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys
405 410 415

Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala
420 425 430

Asp Asp Ile Ser Leu Leu Lys
435

<210> 70
<211> 390
<212> PRT
<213> Homo sapiens

<400> 70

Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu
1 5 10 15

Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr
20 25 30

Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His
35 40 45

Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys
50 55 60

Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly
65 70 75 80

Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala
85 90 95

Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser

100	105	110
Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro 115 120 125		
Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His 130 135 140		
Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu 145 150 155 160		
Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly 165 170 175		
Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile 180 185 190		
Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn 195 200 205		
Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser 210 215 220		
Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe 225 230 235 240		
Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe 245 250 255		
Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly 260 265 270		
Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly 275 280 285		
Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr 290 295 300		
Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys 305 310 315 320		
Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile 325 330 335		
Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly 340 345 350		

Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala
 355 360 365

Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn
 370 375 380

Ile Pro Gln Thr Asp Glu
 385 390

<210> 71
 <211> 374
 <212> PRT
 <213> Homo sapiens
 <400> 71

Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
 1 5 10 15

Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val
 20 25 30

Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp
 35 40 45

Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu
 50 55 60

His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg
 65 70 75 80

Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu
 85 90 95

Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg
 100 105 110

Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly
 115 120 125

Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg
 130 135 140

Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr
 145 150 155 160

His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro
 165 170 175
 Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile
 180 185 190
 Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro
 195 200 205
 Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile
 210 215 220
 Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys
 225 230 235 240
 Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val
 245 250 255
 Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys
 260 265 270
 Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala
 275 280 285
 Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met
 290 295 300
 Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln
 305 310 315 320
 Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr
 325 330 335
 Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val
 340 345 350
 Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile
 355 360 365
 Gly Phe Ala Val Ser Ala
 370

<210> 72
 <211> 14
 <212> PRT
 <213> Artificial

<220>
<223> P10-P4' staD-V peptide inhibitor

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> X is statine moiety

<400> 72

Lys Thr Glu Glu Ile Ser Glu Val Asn Xaa Val Ala Glu Phe
1 5 10

<210> 73
<211> 9
<212> PRT
<213> Artificial

<220>
<223> P4-P4' staD-V peptide inhibitor

<220>
<221> MOD_RES
<222> (1)..(9)
<223> Xaa is statine moiety

<400> 73

Ser Glu Val Asn Xaa Val Ala Glu Phe
1 5

<210> 74
<211> 431
<212> PRT
<213> Homo sapiens

<400> 74

Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala
1 5 10 15

Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu
20 25 30

Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly
35 40 45

Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro
50 55 60

Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val
65 70 75 80

Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe
325 330 335

Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val
340 345 350

Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser
355 360 365

Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val
370 375 380

Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His
385 390 395 400

Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr
405 410 415

Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu
420 425 430

<210> 75
<211> 361
<212> PRT
<213> Homo sapiens

<400> 75

Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu
1 5 10 15

Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr
20 25 30

Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His
35 40 45

Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys
50 55 60

Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly
65 70 75 80

Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala
85 90 95

Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser
100 105 110

Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro
 115 120 125

Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His
 130 135 140

Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu
 145 150 155 160

Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly
 165 170 175

Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile
 180 185 190

Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn
 195 200 205

Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser
 210 215 220

Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe
 225 230 235 240

Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe
 245 250 255

Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly
 260 265 270

Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly
 275 280 285

Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr
 290 295 300

Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys
 305 310 315 320

Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile
 325 330 335

Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly
 340 345 350

Phe Ala Val Ser Ala Cys His Val His
355 360

<210> 76
<211> 63
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(63)
<223> N = A, C, G, or T

<400> 76
garacngayg argarccnga rgarccnggn mgnmgnggnw snttygtnga ratggtngay 60
aay 63

<210> 77
<211> 21
<212> PRT
<213> Homo sapiens

<400> 77

Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
1 5 10 15

Glu Met Val Asp Asn
20

<210> 78
<211> 7
<212> PRT
<213> Artificial

<220>
<223> Peptide inhibitor P3-p4' XD-V

<220>
<221> misc_feature
<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<400> 78

Val Met Xaa Val Ala Glu Phe
1 5

<210> 79
<211> 11
<212> PRT
<213> Homo sapiens

<400> 79

Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
1 5 10

<210> 80

<211> 419

<212> DNA

<213> Artificial

<220>

<223> Nucleotide insert in pCF vector

<400> 80

ctgttgggct cgcggttgag gacaaactct tcgcggtctt tccagtactc ttggatcgga 60
aaccgcgcgg cctccgaacg gtactccgcc accgagggac ctgagcgagt ccgcatcgac 120
cggatcgga aacctctcga ctgttggggg gagtactccc tctcaaaagc gggcatgact 180
tctgcgctaa gattgtcagt ttccaaaaac gaggaggatt tgatattcac ctggcccgcg 240
gtgatgcctt tgagggtggc cgcgtccatc tggtcagaaa agacaatctt tttgttgtea 300
agcttgaggt gtggcaggct tgagatctgg ccatacactt gaggagacaat gacatccact 360
ttgcctttct ctccacaggt gtccactccc aggtccaact gcaggtcgac tctagaccc 419

<210> 81

<211> 408

<212> PRT

<213> Artificial

<220>

<223> pBS/MuImPain E17 #11 construct

<220>

<221> MISC_FEATURE

<222> (1)..(408)

<223> X is hydroxyethylene or statine

<400> 81

Ser Ile Ser Leu Ile Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met
1 5 10 15

Val Asn Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met
20 25 30

Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly
35 40 45

Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg
50 55 60

Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly
65 70 75 80

Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr
85 90 95

Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn
100 105 110

Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn
115 120 125

Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp
130 135 140

Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Ile
145 150 155 160

Pro Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn
165 170 175

Gln Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly
180 185 190

Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg
195 200 205

Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly
210 215 220

Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile
225 230 235 240

Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu
245 250 255

Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro
260 265 270

Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr
275 280 285

Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu
290 295 300

Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu
305 310 315 320

Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe
325 330 335

Ala Val Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met
340 345 350

Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe
355 360 365

Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val
370 375 380

Glu Gly Pro Phe Val Thr Ala Asp Met Glu Asp Cys Gly Tyr Asn Asn
385 390 395 400

Arg Ile Pro Ala Ala Arg Gly Ile
405

<210> 82
<211> 401
<212> PRT
<213> Artificial

<220>
<223> pBS/MuImPain E17 #14 construct

<400> 82

Lys Leu Asp Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp
1 5 10 15

Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val
20 25 30

Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser
35 40 45

Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr Tyr
50 55 60

Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr
65 70 75 80

Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu
85 90 95

Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala
100 105 110

Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu
115 120 125

Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser
130 135 140

Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Ile Pro Asn
145 150 155 160

Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Thr
165 170 175

Glu Ala Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp
180 185 190

His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu
195 200 205

Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp
210 215 220

Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp
225 230 235 240

Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala
245 250 255

Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly
260 265 270

Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro
275 280 285

Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr
290 295 300

Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro
305 310 315 320

Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Val
325 330 335

Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly
340 345 350

Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val
355 360 365

Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly
370 375 380

Pro Phe Val Thr Ala Asp Met Glu Asp Cys Gly Tyr Asn Asn Arg Ile
385 390 395 400

Gln

<210> 83
<211> 231
<212> PRT
<213> Artificial

<220>
<223> pBS/MuImpain E17 Brain #17 construct

<400> 83

Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr
1 5 10 15

Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu
20 25 30

Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro
35 40 45

Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp
50 55 60

Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly
65 70 75 80

Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr
85 90 95

Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Val
100 105 110

Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile
115 120 125

Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys
 130 135 140

Gln Thr His Ile Pro Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly
 145 150 155 160

Phe Pro Leu Asn Gln Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met
 165 170 175

Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr
 180 185 190

Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val
 195 200 205

Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr
 210 215 220

Asp Lys Ser Ile Val Asp Ser
 225 230

<210> 84
 <211> 380
 <212> PRT
 <213> Artificial

<220>
 <223> pBS/ MuImPain E17 Brain #15 construct

<400> 84

Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr
 1 5 10 15

Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu
 20 25 30

Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro
 35 40 45

Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp
 50 55 60

Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly
 65 70 75 80

Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr

				85					90					95			
Val	Arg	Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile		
			100					105					110				
Asn	Gly	Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile		
		115					120					125					
Ala	Arg	Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys		
	130					135					140						
Gln	Thr	His	Ile	Pro	Asn	Ile	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly		
145					150					155					160		
Phe	Pro	Leu	Asn	Gln	Thr	Glu	Ala	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met		
				165					170					175			
Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr		
			180					185					190				
Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val		
		195					200					205					
Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr		
	210					215					220						
Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys		
225					230					235					240		
Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr		
				245					250					255			
Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp		
			260					265					270				
Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr		
		275					280					285					
Leu	Met	Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro		
	290					295					300						
Gln	Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp		
305					310					315				320			
Cys	Tyr	Lys	Phe	Ala	Val	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly		
				325					330					335			

Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys
340 345 350

Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg
355 360 365

Thr Ala Ala Val Glu Gly Pro Phe Val Thr Ala Asp
370 375 380

<210> 85
<211> 427
<212> PRT
<213> Artificial

<220>
<223> pBS/MuImPain H#3 construct

<400> 85

Ile Asp Lys Leu Asp Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met
1 5 10 15

Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met
20 25 30

Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly
35 40 45

Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg
50 55 60

Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly
65 70 75 80

Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr
85 90 95

Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn
100 105 110

Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn
115 120 125

Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp
130 135 140

Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Ile

145		150		155		160
Pro Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn	165		170		175	
Gln Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly	180		185		190	
Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg	195		200		205	
Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly	210		215		220	
Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile	225		230		235	240
Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu	245		250		255	
Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro	260		265		270	
Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr	275		280		285	
Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu	290		295		300	
Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu	305		310		315	320
Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe	325		330		335	
Ala Val Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met	340		345		350	
Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe	355		360		365	
Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val	370		375		380	
Glu Gly Pro Phe Val Thr Ala Asp Met Glu Asp Gly Tyr Asn Asn Arg	385		390		395	400

Ile Pro Ala Ala Arg Gly Ile His Phe Ser Gly Arg His Arg Gly Gly
405 410 415

Ala Pro Ile Arg Pro Ile Val Ser Arg Ile Asn
420 425

<210> 86
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Wild type APP substrate fragment

<400> 86

Val Lys Met Asp
1

<210> 87
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Swedish APP substrate fragment

<400> 87

Val Asn Leu Asp
1

<210> 88
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Human brain N terminus sequence

<400> 88

Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg
1 5 10

<210> 89
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Recombinant 293T N terminus sequence

<400> 89

Thr Gln His Gly Ile Arg Leu Pro Leu Arg
1 5 10

<210> 90
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Recombinant 293T N terminus sequence

<400> 90

Met Val Asp Asn Leu Arg Gly Lys Ser
1 5

<210> 91
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Recombinant CosA2 N terminus sequence

<400> 91

Gly Ser Phe Val Glu Met Val Asp Asn Leu
1 5 10

<210> 92
<211> 10
<212> PRT
<213> Artificial

<220>
<223> 10 peptide sequence with Swedish mutation of APP

<400> 92

Ser Glu Val Asn Leu Asp Ala Glu Phe Arg
1 5 10

<210> 93
<211> 8
<212> PRT
<213> Artificial

<220>
<223> Protein composition containing a beta-secretase inhibitor molecule

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> X = hydrogen, acetyl, t-butoxycarbonyl or carbobenzoyl

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> X = methionine, phenylglycine, n-leucine, asparagine,
 phenylalanine, glycine or valine

 <220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> X = statine, acha(cyclohexylmethylstatine) or phenylstatine
 (Phe-sta) wherein the phenyl group may optionally have mono or
 di-substitution chosen from the group consisting of Cl, F, Br,
 methyl or methoxy.

 <220>
 <221> MISC_FEATURE
 <222> (5)..(5)
 <223> X = valine, alpha-aminobutyric acid, phenylglycine, or alanine

 <400> 93

Xaa Val Xaa Xaa Xaa Ala Glu Phe
 1 5

<210> 94
 <211> 8
 <212> PRT
 <213> Artificial

<220>
 <223> Protein composition containing a beta-secretase inhibitor
 molecule

<220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> X is hydrogen, acetyl, t-butoxycarbonyl or carbobenzoyl

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> X is methionine, phenylglycine, n-leucine, asparagine,
 phenylalanine, glycine or valine.

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> X is statine, acha(cyclohexylmethylstatine) or phenylstatine

<400> 94

Xaa Val Met Xaa Val Ala Glu Phe
 1 5

<210> 95
 <211> 7
 <212> PRT

<213> Artificial

 <220>
 <223> Protein composition containing a beta-secretase inhibitor molecule

 <220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> Valine is acetylated

 <220>
 <221> MISC_FEATURE
 <222> (2)..(2)
 <223> X is phenylglycine

 <220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> X is statine

 <400> 95

 Val Xaa Xaa Val Ala Glu Phe
 1 5

 <210> 96
 <211> 8
 <212> PRT
 <213> Artificial

 <220>
 <223> Protein composition containing a beta-secretase inhibitor molecule

 <220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> X is hydrogen, acetyl, t-butoxycarbonyl or carbobenzoyl

 <220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> X is statine

 <400> 96

 Xaa Val Leu Xaa Val Ala Glu Phe
 1 5

 <210> 97
 <211> 8
 <212> PRT
 <213> Artificial

 <220>
 <223> Protein composition containing a beta-secretase inhibitor

molecule

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> X is hydrogen, acetyl, t-butoxycarbonyl or carbobenzoyl

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> X is statine

<400> 97

Xaa Val Asn Xaa Val Ala Glu Phe
1 5

<210> 98
<211> 8
<212> PRT
<213> Artificial

<220>
<223> Protein composition containing a beta-secretase inhibitor molecule

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> X is hydrogen, acetyl, t-butoxycarbonyl or carbobenzoyl

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> X is statine

<400> 98

Xaa Val Phe Xaa Val Ala Glu Phe
1 5

<210> 99
<211> 6
<212> PRT
<213> Artificial

<220>
<223> Protein composition containing a beta-secretase inhibitor molecule

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> X is phenylstatine

<400> 99

Met Xaa Val Ala Glu Phe
1 5

<210> 100
<211> 8
<212> PRT
<213> Artificial

<220>
<223> Protein composition containing a beta-secretase inhibitor molecule

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> X is Acetyl group

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> X is statine

<400> 100

Xaa Val Met Xaa Val Ala Glu Phe
1 5

<210> 101
<211> 22
<212> DNA
<213> Homo sapiens

<400> 101
cggccggagg ggcagctttg tg

22